Bathyacmaea becki, a new species of pectinodontid limpet (Gastropoda: Pectinodontidae) from a hydrothermal vent of the Manus Back-Arc Basin

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ABSTRACT

A new western Pacific species of the deep-sea limpet family Pectinodontidae is described from hydrothermal vents in Manus Back-Arc Basin, at depths of 1714–1853 m. *Bathyacmea becki* new species is most similar by shell morphology to its geographically closest congener *Bathyacmaea jonassoni* Beck, 1996. However, the new species is characterized by a radula with widened functional lateral teeth, which separates it from other congeners. Phylogenetic reconstructions based respectively on partial sequences of COI and 16S rRNA also support its placement within *Bathyacmea*.

Additional Keywords: Patellogastropoda, chemosynthetic environment, radula, deep-sea

INTRODUCTION

The Manus Basin is one of the best known hydrothermal vent areas in the western Pacific, occupying a back-arc position with respect to the New Britain arc-trench system and containing an active plate boundary (Both et al., 1986). To date, the gastropod fauna of this area has been studied by various authors (e.g., Desbruyères and Laubier, 1989; Beck; 1991; 1992a; 1992b; 1993; Bouchet and Warén, 1991; Warén and Bouchet, 1993). During these studies more than a dozen species have been reported (for reviews see Warén and Bouchet, 2001; Sasaki et al., 2010).

Pectinodontidae Pilsbry, 1891 is a family of deep-sea limpets inhabiting chemosynthetic environments (*Bathyacmaea* Okutani, Tsuchida and Fujikura, 1992 and *Serradonta* Okutani, Tsuchida and Fujikura, 1992, for review see Sasaki et al., 2010) and sunken wood (*Pectinodonta* Dall, 1882, for review see Marshall, 1985; Marshall et al., 2016). Species of *Bathyacmaea* are restricted to the western Pacific region. The group so far consists of six recognized species, known from the Edison Seamount (Beck, 1996), Sagami Bay of Japan (Okutani et al., 1992), Okinawa Trough (Okutani et al., 1993; Sasaki et al., 2003), Nankai Trough (Sasaki et al., 2003) and South China Sea (Zhang et al., 2016).

In the present study, we describe one additional species of *Bathyacmaea*, which was collected by ROV Faxian and a Television Grab (based on mother ship R/V Kexue) during a research cruise carried out by Institute of Oceanology, Chinese Academy of Sciences (IOCAS) in 2015. *Bathyacmaea jonassoni* Beck, 1996 from the Edison Seamount represents the geographically closest taxon to the new species.

MATERIALS AND METHODS

A total of 28 specimens (see Table 1) was collected during several dives of the ROV Faxian and Television Grab (IOCAS) from hydrothermal vent fields, the Pacmanus field (Binns and Wheller, 1991) and Desmos cauldron field (Tufar, 1990). For more detailed information about these sites, see Hashimoto et al. (1999) and Fourre et al. (2006). The materials were fixed in 99.5% ethanol immediately after collection.

Light and Scanning Electron Microscopy: The shell and soft parts were observed under light microscopy, and the radulae using a scanning electron microscope (SEM). For SEM studies, radular sacs were removed and placed in a 10% NaOH solution for 4–5 hours. The radulae were then dehydrated through an ethanol series and laid on a cover slip to air-dry. Samples were coated with gold and examined under a Hitachi S-3400N scanning electron microscope. Type materials were deposited at the Marine Biological Museum, Chinese Academy of Sciences (MBMCAS), Qingdao, China.

Molecular Procedures: Three specimens of *Bathyacmaea becki* new species and one specimen of *Bathyacmaea lactea* Zhang, Zhang, and Zhang, 2016 were subjected to molecular analysis. Genomic DNA was extracted with the Column Genomic DNA Isolation Kit (Beijing TIANGEN, China) according to the manufacturer's instructions. DNA were eluted in elution buffer and stored at –20°C until use.

Table 1. Shell measurements (in mm) and ratios of ***Bathyacmaea becki* new species.**

	Collecting condition	Length (L)	Height (H)	Width (W)	L/H ratio	L/W ratio
Holotype	live	17.9	8.6	15.8	2.1	1.1
Paratypes #1	live	17.3	7.4	14.6	2.3	1.2
Paratypes #2	live	13.8	6.2	10.4	2.2	1.3
Paratypes #3	live	11.7	5.8	8.8	2.0	1.3
Paratypes #4	live	15.0	7.3	12.2	2.1	1.2
Paratypes #5	live	10.2	3.8	8.1	2.7	1.3
Paratypes #6	live	9.7	4.5	7.4	2.2	1.3
Paratypes #7	live	8.9	4.0	6.6	2.2	1.3
Paratypes #8	live	11.1	4.1	8.6	2.7	1.3
Paratypes #9	shell only	15.0	5.8	11.8	2.6	1.3
Paratypes #10	shell only	15.6	6.9	12.9	2.3	1.2
Paratypes #11	shell only	16.1	6.7	13.2	2.4	1.2
Paratypes #12	shell only	15.4	6.8	12.5	2.3	1.2
Paratypes #13	shell only	11.0	4.7	8.0	2.3	1.4
Paratypes #14	live	11.9	5.6	8.5	2.1	1.4
Paratypes #15	live	12.3	5.1	9.4	2.4	1.3
Paratypes #16	live	12.2	5.0	9.2	2.4	1.3
Paratypes #17	live	16.1	7.2	12.0	2.2	1.3
Paratypes #18	live	14.4	5.1	10.9	2.8	1.3
Paratypes #19	live	11.1	4.1	8.4	2.7	1.3
Paratypes #20	live	13.6	5.9	10.6	2.3	1.3
Paratypes #21	live	15.0	5.6	10.4	2.7	1.4
Paratypes #22	live	15.4	6.3	12.9	2.4	1.2
Paratypes #23	live	14.9	5.8	12.5	2.6	1.2
Paratypes #24	live	14.7	5.8	11.6	2.5	1.3
Paratypes #25	live	15.8	6.8	12.2	2.3	1.3
Paratypes #26	live	13.2	5.0	10.9	2.6	1.2
Paratypes #27	live	13.0	5.0	9.8	2.6	1.3

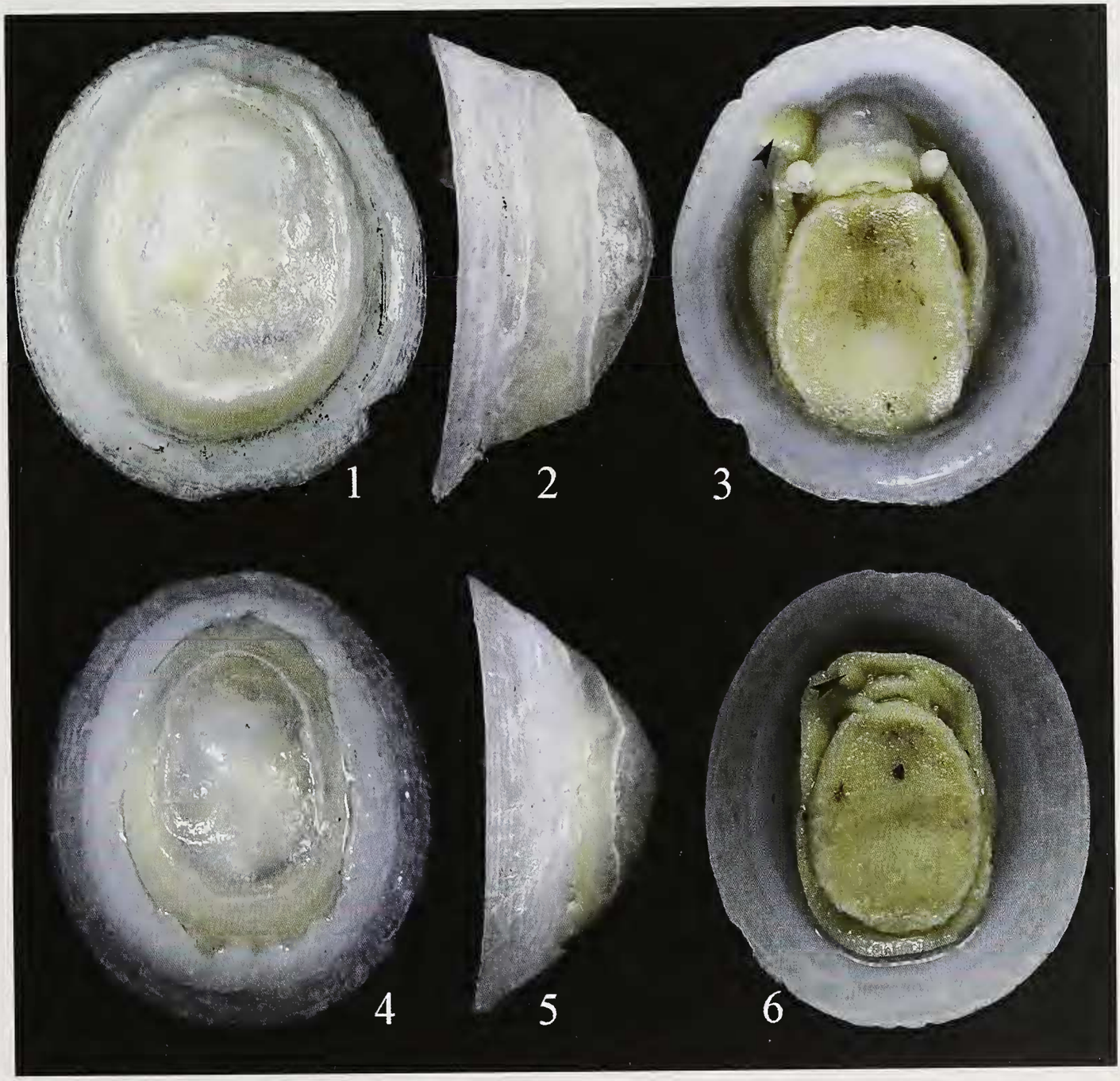
The COI region was amplified by polymerase chain reaction (PCR) using the primers LCO1490 (forward: 5′-GGTCAA CAAATCATAAAGATATTGG-3′) and HCO2198 (reverse: 5′-TTAACTTCAGGGTGACCAAAAAATCA-3′) (Folmer et al., 1994); the 16S rRNA region was amplified using the primers 16Sar (forward: 5′-CGCCTGTTTATCAAAAACAT′) and 16Sbr (reverse: 5′-CCGGTCTGAACTCAGATCACGT-3′) (Palumbi, 1996). PCR reactions were carried out in a total volume of 50 μL, including 1.5 mM $MgCl_2$, 0.2 mM of each dNTPs, 1 μM of both forward and reverse PCR primers, 10×buffer, and 2.5 U Taq DNA polymerase. Thermal cycling was performed under the following conditions: 95°C for 3 min (initial denaturation), followed by 35 cycles of 95°C for 30s (denaturation), annealing temperature for 30s (42°C for COI; 45°C for 16S rRNA), 72°C for 60s (extension), and a final extension at 72°C for 10 min. PCR products were verified by a GelRed-stained 1.5% agarose gel and purified with the Column PCR Product Purification Kit (Shanghai Sangon, China). Purified products were sequenced in both directions. For phylogenetic analyses, COI and 16S rRNA sequences from the present study and those from GenBank were employed (see Table 2, 3). Neighbor-joining (NJ) trees were determined via MEGA 6.06 (Tamura et al., 2013), using Kimura 2-parameter (K2P) model (Kimura, 1980). Bootstrap analyses were performed with 1000 replications.

Table 2. Works from which the COI sequences derived.

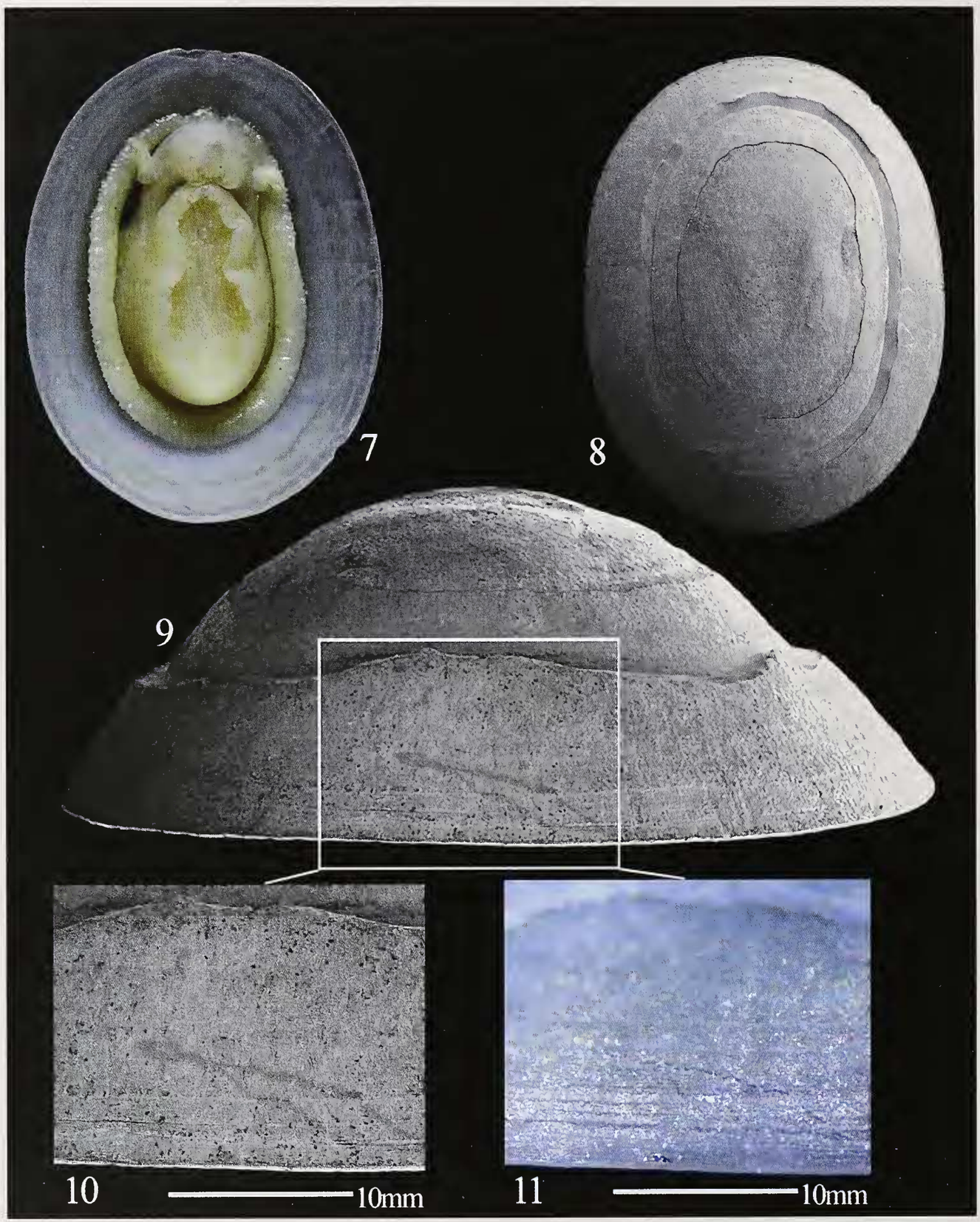
Genus	Species	Accession number	Reference
Bathyacmaea	***Bathyacmaea becki***	MG253685	this study
	Bathyacmaea lactea	MG253686	this study
	Bathyacmaea nipponica	AB238588.1	Nakano and Ozawa, 2007
Pectinodonta	*Pectinodonta aupouria*	KC990591.1	Marshall et al., 2016
	Pectinodonta marinovichi	KC990594.1	Marshall et al., 2016
	Pectinodonta orientalis	KC970665.1	Marshall et al., 2016
	Pectinodonta rhyssa	AB238589.1	Nakano and Ozawa, 2007
***Paralepetopsis* (outgroup)**	*Paralepetopsis* sp.	FJ977752.1	Aktipis and Giribet, 2010

Table 3. Works from which the 16S rRNA sequences derived.

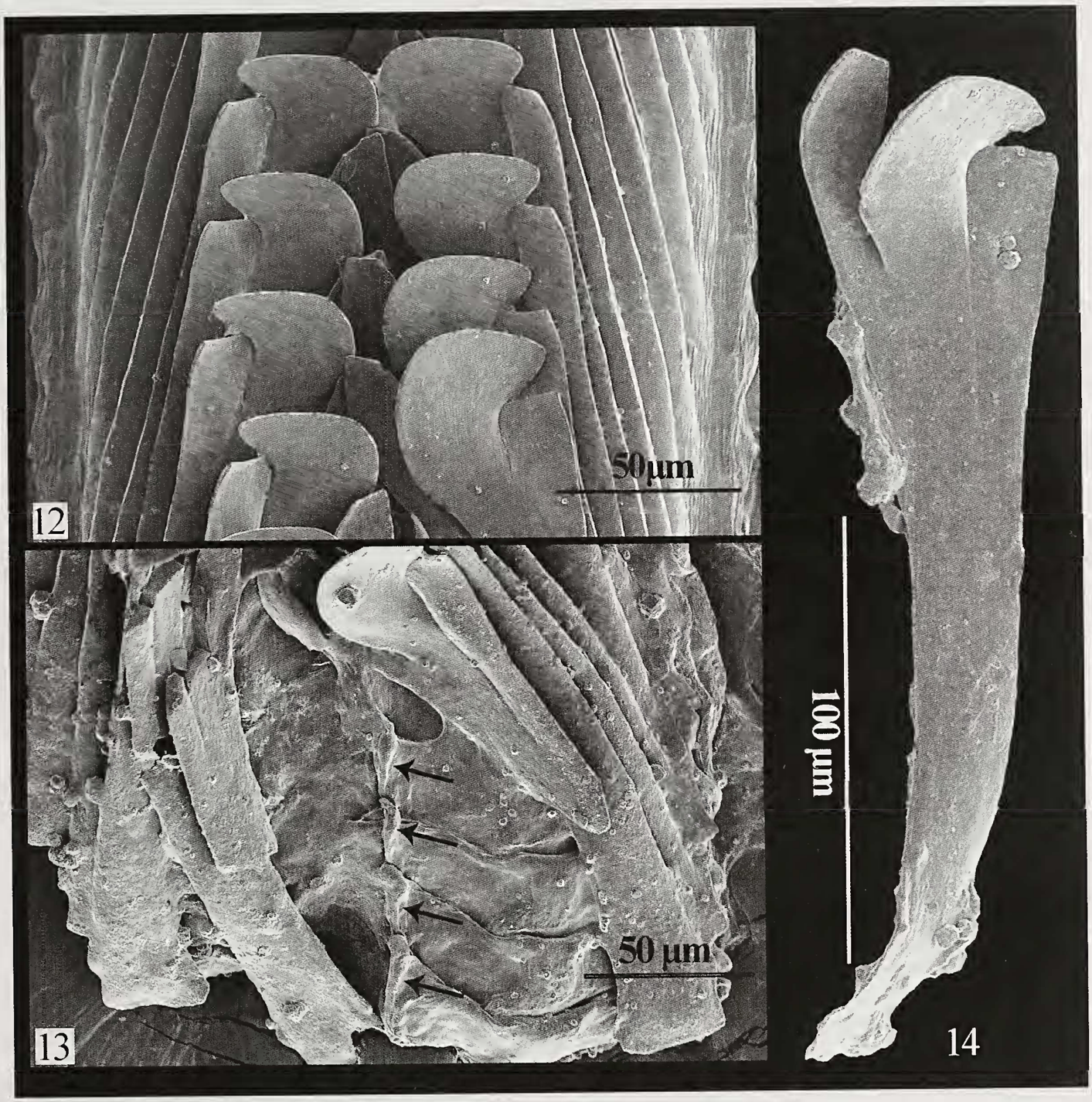
Genus	Species	Accession number	Reference
Bathyacmaea	***Bathyacmaea becki***	MF499155	this study
	Bathyacmaea lactea	MG265696	this study
	Bathyacmaea nipponica	AB238451.1	Nakano and Ozawa, 2007
Pectinodonta	*Pectinodonta rhyssa*	AB238452.1	Nakano and Ozawa, 2007
	Pectinodonta sp.	AY163392.1	Warén et al., 2003
	Pectinodonta sp.	AY160667.1	Aktipis and Giribet, 2012
Paralepetopsis (outgroup)	*Paralepetopsis* sp.	FJ977699.1	Aktipis and Giribet, 2010



Figures 1–6. ***Bathyacmaea becki* new species.** Shells. **1**. Dorsal, **2**. Left lateral, and **3**. Ventral view of the Holotype, 17.9 mm. **4**. Dorsal, **5**. Left lateral, and **6**. Ventral view of Paratype 1, 17.3 mm.



Figures 7–11. ***Bathyacmaea becki*** **new species. 7.** Ventral view of Paratype 2. **8.** Dorsal and, **9.** Lateral view of Paratype 7. **10.** Shell margin under SEM and, **10.** Under light microscopy, showing microsculpture.



Figures 12–14. ***Bathyacmaea becki* new species.** Radula. **12.** Dorsal view of intact radular segment. **13.** Rachidian region, arrows indicate vestigial rachidian teeth. **14.** Single lateral tooth.

Abbreviations: CN: collection number; 16S rRNA: 16S ribosomal RNA; MBM: Marine Biological Museum; RN: Registration number.

SYSTEMATICS

Family Pectinodontidae Pilsbry, 1891

Genus *Bathyacmaea* Okutani, Tsuchida, and Fujikura, 1992

Type Species: *Bathyacmaea nipponica* Okutani, Tsuchida, and Fujikura, 1992 (off Hatsushima Islet, Sagami Bay, Japan, between depths of 1110–2000 m).

***Bathyacmaea becki* new species**
(Figures 1–16)

Diagnosis: Shell whitish, thin, semi-transparent. Shell surface sculptured with obsolete, concentric growth lines, crossed by very faint axial ridges. Aperture oval to nearly

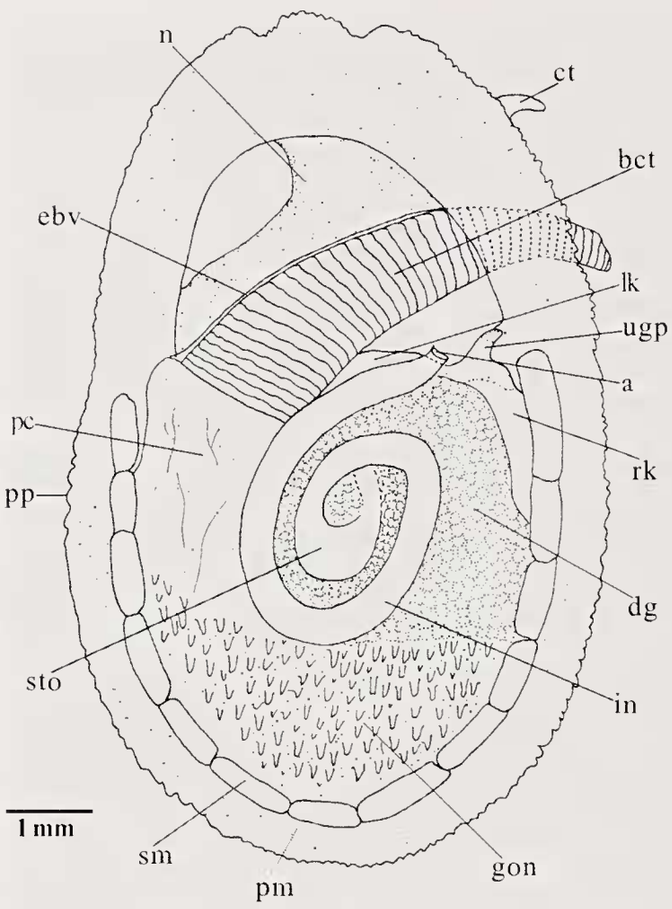


Figure 15. ***Bathyacmaea becki* new species.** Dorsal view of soft parts of Paratype 2, with mantle skirt removed. Abbreviations: **a:** anus; **bct:** bipectinate ctenidium; **ct:** cephalic tentacle; **dg**: digest gland; **ebv:** efferent branchial vein; **gon:** gonad; **in:** intestine; **lk:** left kidney; **n:** neck; **pc:** pericardium; **pm:** pallial margin; **pp:** pallial papillae; **rk:** right kidney; **sm:** shell muscle; **sto**: stomach; **ugp:** urogenital papilla.

rounded in shape, anterior end slightly narrower. Radula formula 0+1+0+1+0, lateral teeth trifurcated, with straight, stout shaft, all three cusps widened, the outermost one with truncated tip.

Description: Shell (Figures 1–11) patelliform, thin (ca. 0.6 mm above aperture margin in holotype), semi-transparent. Outline oval to nearly rounded, longer than wide, width 71–91% (mean 78%) of the length, anterior end slightly narrower than posterior end. Profile high for genus, height 36–50% (mean 42%) of the shell length. Apex on mid-line slightly anterior to center of shell, moderately eroded, protoconch not preserved. All slopes convex, with prominent constriction at transition to thickened peristoma. External surface whitish, sculptured consisting of concentric growth lines, crossed by very faint axial ridge (Figures 9, 10, 11). Aperture slightly concave at sides; margin thickened, slightly reflected.

Soft Parts (Figures 3, 6, 7, 15):

Head rounded, stout. Cephalic tentacles short, tapering. Eyes and oral lappets lacking. Foot sole large, ovate in shape, anterior pedal gland lacking, no obvious epipodium; mantle edge with numerous papillae, more developed in juveniles (Figure 7). Ctenidium bipectinate, large, usually extending out of the mantle cavity (Figures 3, 6, arrows). Radular sac not very long for a patellogastropod, extending from buccal cavity straight to middle part of visceral mass (at level of stomach), where it turns to right to form large loop. Posterior part of radular sac entirely embedded in digestive gland. Intestine blackish due to dark-gray contents. Stomach moderately large, C-shaped, situated in central position of visceral mass. Intestine and stomach containing soft, lumpish material. Gonad situated posteriorly to visceral mass. Urogenital papilla digitiform, situated right-anteriorly to visceral mass. Pericardium (Figure 15) situated left-anteriorly to corner of visceral mass. Left kidney very small, located to right of pericardium, between basal gill and rectum. Pericardium separated from left kidney, as in some patellogastropods, i.e. Acmaeidae, Lottiidae, and Neolepetopsidae. Right kidney more developed, situated at right anterior corner of visceral mass.

Radula (Figures 12–14):

Docoglossate with formula 0+1+0+1+0. Lateral tooth trifurcated, with straight, stout shaft. Single lateral tooth ca. 220 μm long. Innermost cusp relatively narrow, with pointed tip; middle cusp spoon-shaped, strongly curved outward; outermost cusp widened, with truncated tip.

Type Locality: Pacmanus hydrothermal vent field, Manus Back-Arc Basin, 3°44′02.329″ S, 151°40′39.419″ E, 1740 m, hard bottom,.

Type Material: Holotype: RN: MBM285093 (length 17.9 mm, width 15.8 mm, height 8.6 mm), CN: M067, Dive 33, 12 June 2015, from type locality; **paratypes 1–3**, RN: MBM285094, CN: M067, collected with the holotype from Fenway vent in Pacmanus field; from type locality; **paratypes 4–8**, RN: MBM285095, CN: M200, collected by Television Grab (TVG) from Fenway vent in Pacmanus field, 3°43.728′ S 151°40.326′ E, 1714 m, hard bottom, 20 June 2015; **paratypes 9–13**, RN: MBM285096, CN: M073, Dive 34, collected from Desmos cauldron field, 3°41′30.352″ S 151°51′56.172″ E, 1921 m, 13 June 2015; **paratypes 14, 15**, RN: MBM285097, CN: M045, Dive 32, collected Satanic Mills vent in Pacmanus field, 3°43′41.660″ S 151°40′09.793″ E, 11 June 2015; **paratype 16**, RN: MBM285098, CN: M022, Dive 31, collected from Desmos cauldron field, 03°43′40.803″ S, 151°40′09.189″ E, 10 June 2015; **paratypes 17–21**, RN: MBM285099, CN: M087, Dive 36, collected from Desmos cauldron field, 03°42′40.206″ S, 151°52′50.368″ E, 14 June 2015; **paratypes 22–27**, RN: MBM285100, CN: M129, Dive 39, collected from Desmos cauldron field, 3°40′54.605″ S, 151°51′47.613″ E, 1853 m, 17 June 2015. All type specimens were

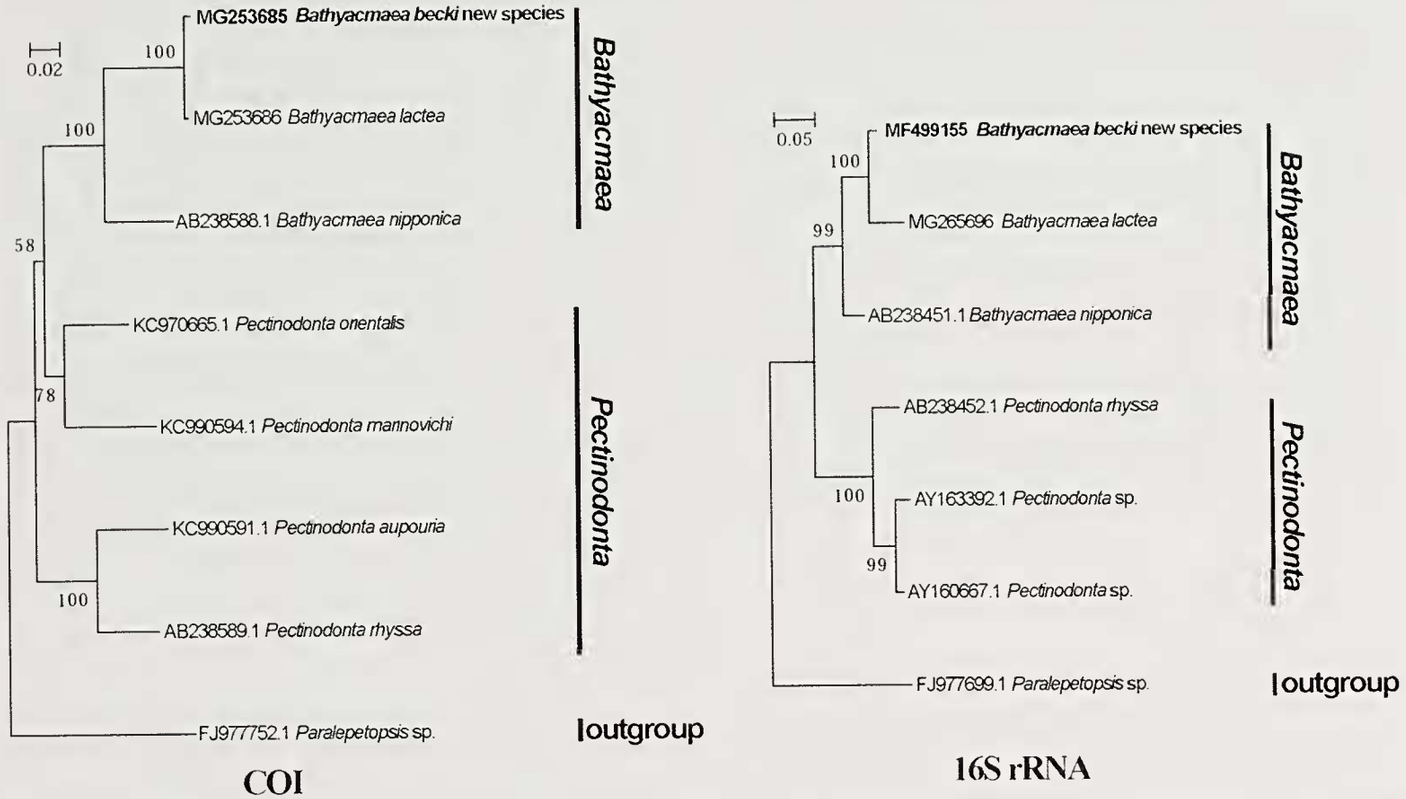


Figure 16. Neighbour-joining trees for Pectinodontidae based on suitable COI and 16S rRNA sequences from GenBank and this study. Numbers above branches indicate the bootstrap values.

collected during the CHINA 1501 Vent Cruise of the R/V KEXUE, via ROV FAXIAN and Television Grab.

Distribution and Habitat: Pacmanus and Desmos cauldron field in the Manus Back-Arc Basin, live on mussels or rock surface, at depths of 1714–1921 m.

Etymology: The new species is named after Dr. Lothar A. Beck, in recognition of his pioneering jobs on the gastropod fauna of hydrothermal vents, especially in the Manus Basin.

Remarks: *Bathyacmaea becki* new species is similar in shell morphology to its geographically closest congener *Bathyacmaea jonassoni* Beck, 1996. However, the new species differs from *B. jonassoni* Beck, 1996 and other congeners by having enlarged lateral teeth with widened cusps of which the outermost one with a truncated tip. In addition, *B. jonassoni* Beck, 1996 has lateral teeth with much longer and thinner shaft. *Bathyacmaea subnipponica* Sasaki, Okutani, and Fujikura, 2003 resembles the new species by its similar radula. However, in *Bathyacmaea subnipponica*, the innermost cusp of the lateral tooth is acute, rather than truncated as in *Bathyacmaea becki*. Moreover, *Bathyacmaea subnipponica* may easily be distinguished from *Bathyacmaea becki* by its shell sculpture with a beaded appearance.

The external anatomy of *Bathyacmaea becki* new species approximates that of *Bathyacmaea jonassoni* Beck, 1996 and *Bathyacmaea secunda* Okutani, Fujikura, and Sasaki, 1993 (see Sasaki et al., 2006). It remarkably differs from them, however, by the shape of the distal end of the urogenital papilla (digitiform in the new species in contrast to bilobed in *Bathyacmaea jonassoni* and *Bathyacmaea secunda*). In addition, the outline of the soft parts of *Bathyacmaea secunda* is more rounded than that of *Bathyacmaea becki* new species.

Examination of the intestine and stomach contents by microscopy revealed some soft, lumpish mass and black mineral particles; no other fragments or remains were observed. The contents may indicate that the new species could feed on bacterial films grazed off from the rock and mussel surfaces where they attach, as occurs with *Bathyacmaea secunda* (see Sasaki et al., 2006). The enlargement of the lateral teeth may make grazing more effective.

Molecular Analyses: Three partial COI sequences (representing a single haplotype) and one 16S rRNA sequence of the *Bathyacmaea becki*, one COI and one 16S rRNA sequences of *Bathyacmaea lactea* were obtained. The sequences have been deposited in GenBank (see Table 2, 3 for accession numbers). The single sequence type obtained from three individuals of the new species is indicative of a high intraspecific conservation of the COI sequence. The Neighbor-joining (NJ) trees (Figure 16) were reconstructed using suitable COI and 16S rRNA sequences from GenBank and this study. The two NJ trees all show that *Bathyacmaea becki* new

species falls into *Bathyacmaea* in which, together with *Bathyacmaea lactea*, it forms a well-supported sister clade to *Bathyacmaea nipponica* Okutani, Tsuchida, and Fujikura, 1992. With available molecular data, the analysis of a 639-bp fragment of the COI gene resulted in 1% pairwise distance between *Bathyacmaea becki* and *Bathyacmaea lactea*, 10% between *Bathyacmaea becki* and *Bathyacmaea nipponica;* whereas the analysis of a 495-bp fragment of the 16S rRNA gene showed a 5% pairwise distance between *Bathyacmaea becki* and *Bathyacmaea lactea* and 7% between *Bathyacmaea becki* and *Bathyacmaea nipponica*. Although the small pairwise distance of COI sequences seems not to separate *Bathyacmaea becki* and *Bathyacmaea lactea*, the 6% pairwise distance of 16S rRNA sequences is enough to warrant a separation of the two species. Morphologically, the two species are evidently different from each other, as evidenced by characters of both shell and radula.

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